

WHAT IS CLAIMED IS:

1. A method of identifying a sequence of a nucleic acid for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising:
  - 5 (a) determining a full length synthesis probability measure for each member sequence of a set of a plurality of candidate probe sequences for said target nucleic acid; and
  - (b) employing said determined full length synthesis probability measures to select a sequence for use as a substrate immobilized probe for said target  
10 nucleic acid.
2. The method according to Claim 1, wherein those sequences of said set that satisfy a full length synthesis probability threshold are selected .
- 15 3. The method according to Claim 2, wherein said full length synthesis probability measure is a measure of the probability that said candidate probe sequence will be fully synthesized by an in situ nucleic acid synthesis protocol.
4. The method according to Claim 3, wherein said full length synthesis  
20 probability measure is an evaluation of said candidate probe sequence's depurination susceptibility during said in situ nucleic acid synthesis protocol.
5. The method according to Claim 4, wherein said depurination susceptibility measure is a deblock dose or parameter based thereon.  
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6. The method according to Claim 5, wherein said method comprises determining a total deblock dose for each member sequence of said set.
7. The method according to Claim 6, wherein said full length synthesis  
30 probability threshold is a total deblock dose threshold and selected sequences have a total deblock dose that does not exceed said deblock dose threshold.

8. The method according to Claim 6, wherein said total deblock dose is a sum of individual deblock doses over all A nucleotides of said candidate probe sequence, except for any 5' terminal A nucleotide.
- 5 9. The method according to Claim 8, wherein each of said individual deblock doses  $d(x)$  for an A nucleotide positioned at layer  $x$  of a candidate probe sequence to be produced by a process having  $L$  total layers is equal to  $L-x+1$ .
- 10 10. The method according to Claim 1, wherein at least some of said steps are carried out by a computational analysis system.
- 15 11. A computer-readable medium having recorded thereon a program that identifies a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid according to the method of Claim 1.
12. A computational analysis system comprising a computer-readable medium according to Claim 11.
- 20 13. A method of producing a nucleic acid array, said method comprising:  
producing at least two different probe nucleic acids immobilized on a surface of a solid support, wherein at least one of said at least two different probe nucleic acids has a sequence of nucleotides identified according to the method of Claim 1.
- 25 14. The method according to Claim 13, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by synthesizing said probe nucleic acids on said surface.
- 30 15. The method according to Claim 13, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by depositing said at least two different probe nucleic acids onto said surface of said solid support.
16. A nucleic acid array produced according to the method of Claim 13.

17. A method of detecting the presence of a nucleic acid analyte in a sample, said method comprising:

(a) contacting a nucleic acid array according to Claim 16 having a nucleic acid probe that specifically binds to said nucleic acid analyte with a sample suspected of comprising said analyte under conditions sufficient for binding of said analyte to said nucleic acid ligand on said array to occur; and

(b) detecting the presence of binding complexes on the surface of said array to detect the presence of said analyte in said sample.

18. A method comprising transmitting a result from a reading of an array according to the method of Claim 17 from a first location to a second location.

19. The method according to Claim 18, wherein said second location is a remote location.

20. A method comprising receiving a transmitted result of a reading of an array obtained according to the method Claim 17.

21. A kit for identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, said kit comprising:

(a) an algorithm that identifies a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for said target nucleic acid according to the method according to Claim 1, wherein said algorithm is present on a computer readable medium; and

(b) instructions for using said algorithm to identify said sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for said target nucleic acid.

22. In a method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, the improvement comprising:

evaluating a plurality of candidate probe sequences for said target nucleic acid for depurination susceptibility.

23. In a method of identifying a sequence of a polymeric ligand for use as a substrate surface immobilized probe, the improvement comprising:
- evaluating a plurality of candidate probe sequences for said polymeric
- 5 ligand for synthesis degradation probability.